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ATGTGGGTGACCAAACCTCTGCCAGCCCTGCTGCTGCAGCATGTCCTCCTGCATCTCCTC  
1 -----+-----+-----+-----+-----+-----+ 60  
TACACCCACTGGTTTGAGGACGGTCGGGACGACGACGTCGTACAGGAGGACGTAGAGGAG  
1 M W V T K L L P A L L L Q H V L L H L L 20  
CTGCTCCCCATCGCCATCCCCTATGCAGAGGGACAAAGGAAAAGAAGAAATACAATTCAT  
61 -----+-----+-----+-----+-----+-----+ 120  
GACGAGGGGTAGCGGTAGGGGATACGTCTCCCTGTTTCCTTTCTTCTTTATGTTAAGTA  
21 L L P I A I P Y A E G Q R K R R N T I H 40  
GAATTCAAAAAATCAGCAAAGACTACCCTAATCAAAATAGATCCAGCACTGAAGATAAAA  
121 -----+-----+-----+-----+-----+-----+ 180  
CTTAAGTTTTTTTAGTCGTTTCTGATGGGATTAGTTTTATCTAGGTCGTGACTTCTATTTT  
41 E F K K S A K T T L I K I D P A L K I K 60  
ACCAAAAAAGTGAATACTGCAGACCAATGTGCTAATAGATGTACTAGGAATAAAGGACTT  
181 -----+-----+-----+-----+-----+-----+ 240  
TGGTTTTTTTCACTTATGACGTCTGGTTACACGATTATCTACATGATCCTTATTTCTGAA  
61 T K K V N T A D Q C A N R C T R N K G L 80  
CCATTCACCTTGCAAGGCTTTTGTTTTTGATAAAGCAAGAAAACAATGCCTCTGGTTCCCC  
241 -----+-----+-----+-----+-----+-----+ 300  
GGTAAGTGAACGTTCCGAAAACAAAACCTATTTTCGTTCTTTTGTTACGGAGACCAAGGGG  
81 P F T C K A F V F D K A R K Q C L W F P 100  
TTCAATAGCATGTCAAGTGGAGTGAAAAAGAATTTGGCCATGAATTTGACCTCTATGAA  
301 -----+-----+-----+-----+-----+-----+ 360  
AAGTTATCGTACAGTTCACCTCACTTTTTTCTTAAACCGGTACTTAACTGGAGATACTT  
101 F N S M S S G V K K E F G H E F D L Y E 120  
AACAAAGACTACATTAGAAACTGCATCATTGGTAAAGGACGCAGCTACAAGGGAACAGTA  
361 -----+-----+-----+-----+-----+-----+ 420  
TTGTTTCTGATGTAATCTTTGACGTAGTAACCATTTCTGCGTCGATGTTCCCTTGTCAT  
121 N K D Y I R N C I I G K G R S Y K G T V 140  
TCTATCACTAAGAGTGGCATCAAATGTCAGCCCTGGAGTTCCATGATACCACACGAACAC  
421 -----+-----+-----+-----+-----+-----+ 480  
AGATAGTGATTCTACCGTAGTTTACAGTCGGGACCTCAAGGTACTATGGTGTGCTTGTG  
141 S I T K S G I K C Q P W S S M I P H E H 160

FIG.1a-1



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AGCTATCGGGGTAAAGACCTACAGGAAAACCTACTGTCGAAATCCTCGAGGGGAAGAAGGG  
481 .....+.....+.....+.....+.....+.....+.....+ 540  
TCGATAGCCCCATTTCTGGATGTCCTTTTGATGACAGCTTTAGGAGCTCCCCTTCTTCCC  
161 S Y R G K D L Q E N Y C R N P R G E E G 180  
GGACCCTGGTGTTCACAAGCAATCCAGAGGTACGCTACGAAGTCTGTGACATTCCTCAG  
541 .....+.....+.....+.....+.....+.....+.....+ 600  
CCTGGGACCACAAAGTGTTTCGTTAGGTCTCCATGCGATGCTTCAGACACTGTAAGGAGTC  
181 G P W C F T S N P E V R Y E V C D I P Q 200  
TGTTCAGAAGTTGAATGCATGACCTGCAATGGGGAGAGTTATCGAGGTCTCATGGATCAT  
601 .....+.....+.....+.....+.....+.....+.....+ 660  
ACAAGTCTTCAACTTACGTACTGGACGTTACCCCTCTCAATAGCTCCAGAGTACCTAGTA  
201 C S E V E C M T C N G E S Y R G L M D H 220  
ACAGAATCAGGCAAGATTTGTGACGCTGGGATCATCAGACACCACACCGGCACAAATTC  
661 .....+.....+.....+.....+.....+.....+.....+ 720  
TGTCTTAGTCCGTTCTAAACAGTCGCGACCCTAGTAGTCTGTGGTGTGGCCGTGTTAAG  
221 T E S G K I C Q R W D H Q T P H R H K F 240  
TTGCCTGAAAGATATCCCGACAAGGGCTTTGATGATAATTATTGCCGCAATCCCGATGGC  
721 .....+.....+.....+.....+.....+.....+.....+ 780  
AACGGACTTTCTATAGGGCTGTTCCCGAACTACTATTAATAACGGCGTTAGGGCTACCG  
241 L P E R Y P D K G F D D N Y C R N P D G 260  
CAGCCGAGGCCATGGTGTCTATACTCTTGACCCTCACACCCGCTGGGAGTACTGTGCAATT  
781 .....+.....+.....+.....+.....+.....+.....+ 840  
GTCGGCTCCGGTACCACGATATGAGAACTGGGAGTGTGGGCGACCCTCATGACACGTAA  
261 Q P R P W C Y T L D P H T R W E Y C A I 280  
AAAACATGCGCTGACAATACTATGAATGACACTGATGTTCTTTGGAAACAACCTGAATGC  
841 .....+.....+.....+.....+.....+.....+.....+ 900  
TTTTGTACGCGACTGTTATGATACTTACTGTGACTACAAGGAAACCTTTGTTGACTTACG  
281 K T C A D N T M N D T D V P L E T T E C 300  
ATCCAAGGTCAAGGAGAAGGCTACAGGGGCACTGTCAATACCATTTGGAATGGAATTCCA  
901 .....+.....+.....+.....+.....+.....+.....+ 960  
TAGGTTCCAGTTCCTCTTCCGATGTCCCGTGACAGTTATGGTAAACCTTACCTTAAGGT  
301 I Q G Q G E G Y R G T V N T I W N G I P 320  
TGTCAGCGTTGGGATTCTCAGTATCCTCACGAGCATGACATGACTCCTGAAAATTTCAAG  
961 .....+.....+.....+.....+.....+.....+.....+ 1020  
ACAGTCGCAACCCTAAGAGTCATAGGAGTGCTCGTACTGTACTGAGGACTTTTAAAGTTC  
321 C Q R W D S Q Y P H E H D M T P E N F K 340  
TGCAAGGACCTACGAGAAAATTACTGCCGAAATCCAGATGGGTCTGAATCACCTGGTGT  
1021 .....+.....+.....+.....+.....+.....+.....+ 1080  
ACGTTCTGGATGCTCTTTTAATGACGGCTTTAGGTCTACCCAGACTTAGTGGGACCACA  
341 C K D L R E N Y C R N P D G S E S P W C 360  
TTTACCACTGATCCAAACATCCGAGTTGGCTACTGCTCCCAAATTCCAAACCTGTGATATG  
1081 .....+.....+.....+.....+.....+.....+.....+ 1140  
AAATGGTGACTAGGTTTGTAGGCTCAACCGATGACGAGGGTTTAAGGTTTGACACTATAC  
361 F T T D P N I R V G Y C G Q I P N C D M 380

FIG.1a-2



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1141 TCACATGGACAAGATTGTTATCGTGGGAATGGCAAAAATTATATGGGCAACTTATCCCAA 1200  
-----+-----+-----+-----+-----+-----+  
AGTGTACCTGTTCTAACAATAGCACCTTACCGTTTTTAATATACCCGTTGAATAGGGTT  
381 S H G Q D C Y R G N G K N Y M G N L S Q 400  
ACAAGATCTGGACTAACATGTTCAATGTGGGACAAGAACATGGAAGACTTACATCGTCAT  
1201 -----+-----+-----+-----+-----+-----+ 1260  
TGTTCTAGACCTGATTGTACAAGTTACACCCTGTTCTTGACCTTCTGAATGTAGCAGTA  
401 T R S G L T C S M W D K N M E D L H R H 420  
ATCTTCTGGGAACCAGATGCAAGTAAGCTGAATGAGAATTACTGCCGAAATCCAGATGAT  
1261 -----+-----+-----+-----+-----+-----+ 1320  
TAGAAGACCCTTGGTCTACGTTTCATTGACTTACTCTTAATGACGGCTTTAGGTCTACTA  
421 I F W E P D A S K L N E N Y C R N P D D 440  
GACGCTCATGGACCCTGGTGTACACGGGAAATCCACTCATTCCCTGGGATTATTGCCCT  
1321 -----+-----+-----+-----+-----+-----+ 1380  
CTGCGAGTACCTGGGACCACGATGTGCCCTTTAGGTGAGTAAGGAACCCTAATAACGGGA  
441 D A H G P W C Y T G N P L I P W D Y C P 460  
ATTTCTCGTTGTGAAGGTGATACCACACCTACAATAGTCAATTTAGACCATCCCCTAATA  
1381 -----+-----+-----+-----+-----+-----+ 1440  
TAAAGAGCAACACTTCCACTATGGTGTGGATGTTATCAGTTAAATCTGGTAGGGCATTAT  
461 I S R C E G D T T P T I V N L D H P V I 480  
TCTTGTGCCAAAACGAAACAATTGCGAGTTGTAAATGGGATTCCAACACGAACAAACATA  
1441 -----+-----+-----+-----+-----+-----+ 1500  
AGAACACGGTTTTGCTTTGTAAACGCTCAACATTTACCCTAAGGTTGTGCTTGTGTTGTAT  
481 S C A K T K Q L R V V N G I P T R T N I 500  
GGATGGATGGTTAGTTTGAGATACAGAAATAAACATATCTGCGGAGGATCATTGATAAAG  
1501 -----+-----+-----+-----+-----+-----+ 1560  
CCTACCTACCAATCAAACCTCTATGTCTTTATTTGTATAGACGCTCCTAGTAACTATTTC  
501 G W M V S L R Y R N K H I C G G S L I K 520  
GAGAGTTGGGTTCTTACTGCACGACAGTGTTCCTTCTCGAGACTTGAAAGATTATGAA  
1561 -----+-----+-----+-----+-----+-----+ 1620  
CTCTCAACCCAAGAATGACGTGCTGTCACAAAGGGAAGAGCTCTGAACCTTCTAATACTT  
521 E S W V L T A R Q C F P S R D L K D Y E 540  
GCTTGGCTTGGAATTCATGATGTCCACGGAAGAGGAGATGAGAAATGCAAACAGGTTCTC  
1621 -----+-----+-----+-----+-----+-----+ 1680  
CGAACCGAACCTTAAGTACTACAGGTGCCTTCTCCTCTACTCTTTACGTTTGTCCAAGAG  
541 A W L G I H D V H G R G D E K C K Q V L 560  
AATGTTTCCCAGCTGGTATATGGCCCTGAAGGATCAGATCTGGTTTTAATGAAGCTTGCC  
1681 -----+-----+-----+-----+-----+-----+ 1740  
TTACAAAGGGTCGACCATATACCGGGACTTCCTAGTCTAGACCAAAATTACTTCGAACGG  
561 N V S Q L V Y G P E G S D L V L M K L A 580  
AGGCCTGCTGTCCTGGATGATTTTGTAGTACGATTGATTTACCTAATTATGGATGCACA  
1741 -----+-----+-----+-----+-----+-----+ 1800  
TCCGGACGACAGGACCTACTAAAACAATCATGCTAACTAAATGGATTAATACCTACGTGT  
581 R P A V L D D F V S T I D L P N Y G C T 600

FIG.1a-3



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1801 ATTCCTGAAAAGACCAGTTGCAGTGTTTATGGCTGGGGCTACACTGGATTGATCAACTAT 1860  
.....+.....+.....+.....+.....+.....+  
TAAGGACTTTTCTGGTCAACGTCACAAATACCGACCCCGATGTGACCTAACTAGTTGATA  
601 I P E K T S C S V Y G W G Y T G L I N Y 620  
GATGGCCTATTACGAGTGGCACATCTCTATATAATGGGAAATGAGAAATGCAGCCAGCAT  
1861 .....+.....+.....+.....+.....+.....+ 1920  
CTACCGGATAATGCTCACCGTGTAGAGATATATTACCTTTACTCTTTACGTCGGTCGTA  
621 D G L L R V A H L Y I M G N E K C S Q H 640  
CATCGAGGGAAGGTGACTCTGAATGAGTCTGAAATATGTGCTGGGGCTGAAAAGATTGGA  
1921 .....+.....+.....+.....+.....+.....+ 1980  
GTAGCTCCCTTCCACTGAGACTTACTCAGACTTTATACACGACCCCGACTTTTCTAACCT  
641 H R G K V T L N E S E I C A G A E K I G 660  
TCAGGACCATGTGAGGGGGATTATGGTGGCCCACTTGTTTGTGAGCAACATAAAATGAGA  
1981 .....+.....+.....+.....+.....+.....+ 2040  
AGTCCTGGTACACTCCCCCTAATACCACCGGGTGAACAAACACTCGTTGTATTTTACTCT  
661 S G P C E G D Y G G P L V C E Q H K M R 680  
ATGGTTCTTGGTGTCAATTGTTCCCTGGTCGTGGATGTGCCATTCCAAATCGTCCTGGTATT  
2041 .....+.....+.....+.....+.....+.....+ 2100  
TACCAAGAACCACAGTAACAAGGACCAGCACCTACACGGTAAGGTTTAGCAGGACCATAA  
681 M V L G V I V P G R G C A I P N R P G I 700  
TTTGTCCGAGTAGCATATTATGCAAAATGGATACACAAAATTATTTTAACATATAAGGTA  
2101 .....+.....+.....+.....+.....+.....+ 2160  
AAACAGGCTCATCGTATAATACGTTTTACCTATGTGTTTTAATAAAATTGTATATTCCAT  
701 F V R V A Y Y A K W I H K I I L T Y K V 720  
CCACAGTCATAG  
2161 .....+--- 2172  
GGTGTCAGTATC  
721 P Q S \* 723

FIG.1a-4

```

1  ATGGGGTGGCTCCCACTCCTGCTGCTTCTGACTCAATGCTTAGGGGTCCCTGGGCAGCGC 60
   +-----+-----+-----+-----+-----+-----+
1  TACCCACCGAGGGTGAGGACGACGAAGACTGAGTTACGAATCCCAGGGACCCGTCGCG 20
   M G W L P L L L L L T Q C L G V P G Q R
61  TCGCCATTGAATGACTTCCAAGTGCTCCGGGGCACRGAGCTACAGCACCTGCTACATGCG
   +-----+-----+-----+-----+-----+-----+ 120
61  AGCGGTAACCTTACTGAAGGTTACGAGGCCCGTGTCTCGATGTCGTGGACGATGTACGC
   S P L N D F Q V L R G T E L Q H L L H A 40
21  GTGGTGCCCGGGCCTTGGCAGGAGGATGTGGCAGATGCTGAAGAGTGTGCTGGTCGCTGT
   +-----+-----+-----+-----+-----+-----+ 180
121  CACCACGGGCCCGGAACCGTCCTCCTACACCGTCTACGACTTCTCACACGACCAGCGACA
   V V P G P W Q E D V A D A E E C A G R C 60
41  GGGCCCTTAATGGAAGTGGCGGGCCTTCCACTACAACGTGAGCAGCCATGGTTGCCAACTG
   +-----+-----+-----+-----+-----+-----+ 240
181  CCCGGGAATTACCTGACGGGCCCGGAAGGTGATGTTGCACTCGTCGGTACCAACGGTTGAC
   G P L M D C R A F H Y N V S S H G C Q L 80
61  CTGCCATGGACTCAACACTCGCCCCACACGAGGCTGCGGCGTTCTGGGCGCTGTGACCTC
   +-----+-----+-----+-----+-----+-----+ 300
241  GACGGTACCTGAGTTGTGAGCGGGGTGTGCTCCGACGCCGAAGACCCGCGACACTGGAG
   L P W T Q H S P H T R L R R S G R C D L 100
81  TTCCAGAAGAAAGACTACGTACGGACCTGCATCATGAACAATGGGGTTGGGTACCGGGGC
   +-----+-----+-----+-----+-----+-----+ 360
301  AAGGTCTTCTTTCTGATGCATGCCTGGACGTAGTACTTGTTACCCCAACCCATGGCCCCG
   F Q K K D Y V R T C I M N N G V G Y R G 120
101  ACCATGGCCACGACCGTGGGTGGCCTGCCCTGCCAGGCTTGAGCCACAAGTTCCCGAAT
   +-----+-----+-----+-----+-----+-----+ 420
361  TGGTACCGGTGCTGGCACCCACCGGACGGGACGGTCCGAACCTCGGTGTTCAAGGGCTTA
   T M A T T V G G L P C Q A W S H K F P N 140
121  GATCACAAGTACACGCCCACTCTCCGGAATGGCCTGGAAGAGAACTTCTGCCGTAACCCT
   +-----+-----+-----+-----+-----+-----+ 480
421  CTAGTGTTTCATGTGCGGGTGAGAGGCCTTACCGGACCTTCTCTTGAAGACGGCATTGGGA
   D H K Y T P T L R N G L E E N F C R N P 160
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FIG.1b-1

FIG. 1b-2



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ACGGTCAGCAAGACCCGCAAGGGTGTCCAGTGCCAGCGCTGGTCCGCTGAGACGCCGCAC  
1141 .....+.....+.....+.....+.....+.....+.....+ 1200  
TGCCAGTCGTTCTGGGCGTTCACAGGTACGGTCGCGACCAGGCGACTCTGCGGCGTG  
381 T V S K T R K G V Q C Q R W S A E T P H 400  
AAGCCGCAGTTCACGTTTACCTCCGAACCGCATGCACAACCTGGAGGAGAACTTCTGCCGG  
1201 .....+.....+.....+.....+.....+.....+.....+ 1260  
TTCGGCGTCAAGTGCAAATGGAGGCTTGGCGTACGTGTTGACCTCCTCTTGAAGACGGCC  
401 K P Q F T F T S E P H A Q L E E N F C R 420  
AACCCAGATGGGGATAGCCATGGGCCCTGGTGCTACACGATGGACCCAAGGACCCCATTC  
1261 .....+.....+.....+.....+.....+.....+.....+ 1320  
TTGGGTCTACCCCTATCGGTACCCGGGACCACGATGTGCTACCTGGGTTCTGGGGTAAG  
421 N P D G D S H G P W C Y T M D P R T P F 440  
GACTACTGTGCCCTGCGACGCTGCGCTGATGACCAGCCGCCATCAATCCTGGACCCCCCA  
1321 .....+.....+.....+.....+.....+.....+.....+ 1380  
CTGATGACACGGGACGCTGCGACGCGACTACTGGTCGGCGGTAGTTAGGACCTGGGGGGT  
441 D Y C A L R R C A D D Q P P S I L D P P 460  
GACCAGGTGCAGTTTGAGAAGTGTGGCAAGAGGGTGGATCGGCTGGATCAGCGGCGTTCC  
1381 .....+.....+.....+.....+.....+.....+.....+ 1440  
CTGGTCCACGTCAAACCTCTTACACCGTTTCTCCACCTAGCCGACCTAGTCGCCGCAAGG  
461 D Q V Q F E K C G K R V D R L D Q R R S 480  
AAGCTGCGCGTGGTTGGGGGCCATCCGGGCAACTACCCTGGACAGTCAGCTTGCGGAAT  
1441 .....+.....+.....+.....+.....+.....+.....+ 1500  
TTCGACGCGCACCAACCCCGGTAGGCCCGTTGAGTGGGACCTGTCAGTCGAACGCCTTA  
481 K L R V V G G H P G N S P W T V S L R N 500  
CGGCAGGGCCAGCATTTCTGCGGGGGTCTCTAGTGAAGGAGCAGTGGATACTGACTGCC  
1501 .....+.....+.....+.....+.....+.....+.....+ 1560  
GCCGTCCCGTCTGTAAGACGCCCCCAGAGATCACTTCCTCGTCACCTATGACTGACGG  
501 R Q G Q H F C G G S L V K E Q W I L T A 520  
CGGCAGTGCTTCTCCTCCTGCCATATGCCTCTCACGGGCTATGAGGTATGGTTGGGCACC  
1561 .....+.....+.....+.....+.....+.....+.....+ 1620  
GCCGTACGAAGAGGAGGACGGTATACGGAGAGTGCCGATACTCCATACCAACCCGTGG  
521 R Q C F S S C H M P L T G Y E V W L G T 540  
CTGTTCCAGAACCCACAGCATGGAGAGCCAAGCCTACAGCGGGTCCCAGTAGCCAAGATG  
1621 .....+.....+.....+.....+.....+.....+.....+ 1680  
GACAAGGTCTTGGGTGTCGTACCTCTCGGTTGCGATGTCGCCAGGGTCATCGGTTCTAC  
541 L F Q N P Q H G E P S L Q R V P V A K M 560  
GTGTGTGGGGCCCTCAGGCTCCCAGCTTGTCTGCTCAAGCTGGAGAGATCTGTGACCCTG  
1681 .....+.....+.....+.....+.....+.....+.....+ 1740  
CACACACCCGGGAGTCCGAGGGTGAACAGGACGAGTTCGACCTCTCTAGACACTGGGAC  
561 V C G P S G S Q L V L L K L E R S V T L 580  
AACCAGCGTGTGGCCCTGATCTGCCTGCCCCCTGAATGGTATGTGGTGCCTCCAGGGACC  
1741 .....+.....+.....+.....+.....+.....+.....+ 1800  
TTGGTCGCACACCGGGACTAGACGGACGGGGGACTTACCATACACCACGGAGGTCCCTGG  
581 N Q R V A L I C L P P E W Y V V P P G T 600

FIG.1b-3



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1801 AAGTGTGAGATTGCAGGCTGGGGTGAGACCAAAGGTACGGGTAATGACACAGTCCTAAAT 1860  
-----+-----+-----+-----+-----+-----+  
TTCACACTCTAACGTCCGACCCCACTCTGGTTTCCATGCCCACTTACTGTGTCAGGATTTA  
601 K C E I A G W G E T K G T G N D T V L N 620  
GTGGCCTTTCTGAATGTTATCTCCAACCAGGAGTGTAACATCAAGCACCGAGGACGTGTG  
1861 -----+-----+-----+-----+-----+-----+ 1920  
CACCGGAAAGACTTACAATAGAGGTTGGTCCTCACATTGTAGTTCGTGGCTCCTGCACAC  
621 V A F L N V I S N Q E C N I K H R G R V 640  
CGGGAGAGTGAGATGTGCACTGAGGGACTGTTGGCCCCTGTGGGGGCCTGTGAGGGTGAC  
1921 -----+-----+-----+-----+-----+-----+ 1980  
GCCCTCTCACTCTACACGTGACTCCCTGACAACCGGGGACACCCCGGACACTCCCACTG  
641 R E S E M C T E G L L A P V G A C E G D 660  
TACGGGGGGCCCACTTGCCTGCTTTACCCACAACCTGCTGGGTCTTGAAGGAATTATAATC  
1981 -----+-----+-----+-----+-----+-----+ 2040  
ATGCCCCCGGGTGAACGGACGAAATGGGTGTTGACGACCCAGGACCTTCCTTAATATTAG  
661 Y G G P L A C F T H N C W V L E G I I I 680  
CCCAACCGAGTATGCGCAAGGTCCCGCTGGCCAGCTGTCTTCACGCGTGTCTCTGTGTTT  
2041 -----+-----+-----+-----+-----+-----+ 2100  
GGGTTGGCTCATACGCGTTCCAGGGCGACCGGTCGACAGAAGTGCGCACAGAGACACAAA  
681 P N R V C A R S R W P A V F T R V S V F 700  
GTGGACTGGATTACAAAGGTCATGAGACTGGGTTAG  
2101 -----+-----+-----+-----+-----+ 2136  
CACCTGACCTAAGTGTTCCAGTACTCTGACCCAATC  
701 V D W I H K V M R L G \* 711

FIG.1b-4





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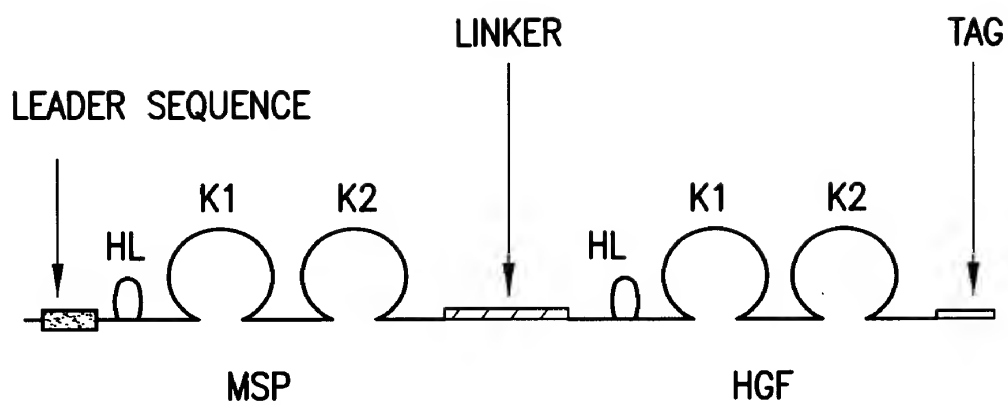


FIG.2a



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GAATTCACCATGGGGTGGCTCCCACTCCTGCTGCTTCTGACTCAATGCTTAGGGGTCCC  
1 .....+.....+.....+.....+.....+.....+.....+ 60  
CTTAAGGTGGTACCCACCGAGGGTGAGGACGACGAAGACTGAGTTACGAATCCCCAGGG  
1 M G W L P L L L L L T Q C L G V P 17  
TGGGCAGCGCTCGCCATTGAATGACTTCCAAGTGCTCCGGGGCACAGAGCTACAGCACCT  
61 .....+.....+.....+.....+.....+.....+.....+ 120  
ACCGTCGCGAGCGGTAACCTACTGAAGGTTACGAGGCCCGTGTCTCGATGTCGTGGA  
18 G Q R S P L N D F Q V L R G T E L Q H L 37  
GCTACATGCGGTGGTGCCCGGGCCTTGGCAGGAGGATGTGGCAGATGCTGAAGAGTGTGC  
121 .....+.....+.....+.....+.....+.....+.....+ 180  
CGATGTACGCCACCACGGGCCCGGAACCGTCCTCCTACACCGTCTACGACTTCTCACACG  
38 L H A V V P G P W Q E D V A D A E E C A 57  
TGGTCGCTGTGGGCCCTTAATGGACTGCCGGGCCCTTCCACTACAACGTGAGCAGCCATGG  
181 .....+.....+.....+.....+.....+.....+.....+ 240  
ACCAGCGACACCCGGGAATTACCTGACGGCCCGGAAGGTGATGTTGCACTCGTCGGTACC  
58 G R C G P L M D C R A F H Y N V S S H G 77  
TTGCCAACTGCTGCCATGGACTCAACACTCGCCCCACACGAGGCTGCGGCGTTCTGGGCG  
241 .....+.....+.....+.....+.....+.....+.....+ 300  
AACGGTTGACGACGGTACCTGAGTTGTGAGCGGGGTGTGCTCCGACGCCGAAGACCCGC  
78 C Q L L P W T Q H S P H T R L R R S G R 97  
CTGTGACCTCTTCCAGAAGAAAGACTACGTACGGACCTGCATCATGAACAATGGGGTTGG  
301 .....+.....+.....+.....+.....+.....+.....+ 360  
GACACTGGAGAAGGTCTTCTTTCTGATGCATGCCTGGACGTAGTACTTGTTACCCCAACC  
98 C D L F Q K K D Y V R T C I M N N G V G 117  
GTACCGGGGCACCATGGCCACGACCGTGGGTGGCCTGCCCTGCCAGGCTTGGAGCCACAA  
361 .....+.....+.....+.....+.....+.....+.....+ 420  
CATGGCCCCGTGGTACCGGTGCTGGCACCCACCGGACGGGACGGTCCGAACCTCGGTGTT  
118 Y R G T M A T T V G G L P C Q A W S H K 137  
GTTCCCGAATGATCACAAGTACACGCCCACTCTCCGGAATGGCCTGGAAGAGAACTTCTG  
421 .....+.....+.....+.....+.....+.....+.....+ 480  
CAAGGGCTTACTAGTGTTTCATGTGCGGGTGAGAGGCCTTACCGGACCTTCTCTTGAAGAC  
138 F P N D H K Y T P T L R N G L E E N F C 157  
CCGTAACCCTGATGGCGACCCCGGAGGTCCTTGGTGCTACACAACAGACCCTGCTGTGCG  
481 .....+.....+.....+.....+.....+.....+.....+ 540  
GGCATTGGGACTACCGCTGGGGCCTCCAGGAACCACGATGTGTTGTCTGGGACGACACGC  
159 R N P D G D P G G P W C Y T T D P A V R 177

FIG.2b-1



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CTTCCAGAGCTGCGGCATCAAATCCTGCCGGGAGGCCGCGTGTGTCTGGTGAATGGCGA  
541 -----+-----+-----+-----+-----+-----+ 600  
GAAGGTCTCGACGCCGTAGTTTAGGACGGCCCTCCGGCGCACACAGACCACGTTACCGCT  
178 F Q S C G I K S C R E A A C V W C N G E 197  
GGAATACCGCGGCGCGGTAGACCGCACGGAGTCAGGGCGCGAGTGCCAGCGCTGGGATCT  
601 -----+-----+-----+-----+-----+-----+ 660  
CCTTATGGCGCCGCGCCATCTGGCGTGCCTCAGTCCC GCGCTCACGGTCGCGACCCTAGA  
198 E Y R G A V D R T E S G R E C Q R W D L 217  
TCAGCACCCGACCCAGCACCCCTTCGAGCCGGGCAAGTTCCTCGACCAAGGTCTGGACGA  
661 -----+-----+-----+-----+-----+-----+ 720  
AGTCGTGGGCGTGGTCGTGGGGAAGCTCGGCCCGTTCAAGGAGCTGGTTCCAGACCTGCT  
218 Q H P H Q H P F E P G K F L D Q G L D D 237  
CAACTATTGCCGGAATCCTGACGGCTCCGAGCGGCCATGGTGCTACACTACGGATCCGCA  
721 -----+-----+-----+-----+-----+-----+ 780  
GTTGATAACGGCCTTAGGACTGCCGAGGCTCGCCGGTACCACGATGTGATGCCTAGGCGT  
238 N Y C R N P D G S E R P W C Y T T D P Q 257  
GATCGAGCGAGAGTTCTGTGACCTCCCCGCTGCGGGTCCGAGGCACAGCCCCGCTCGA  
781 -----+-----+-----+-----+-----+-----+ 840  
CTAGCTCGCTCTCAAGACACTGGAGGGGGCGACGCCAGGCTCCGTGTCGGGGCGGAGCT  
258 I E R E F C D L P R C G S E A Q P R L E 277  
GGGCGGTGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTCTAGAGGGACAAAG  
841 -----+-----+-----+-----+-----+-----+ 900  
CCCGCCACCGCCAAGACCACCGCCACCGAGGCCGCCACCGCCAAGAGATCTCCCTGTTTC  
278 G G G G S G G G G S G G G G S L E G Q R 297  
GAAAAGAAGAAATACAATTCATGAATTCAAAAATCAGCAAAGACTACCCTAATCAAAAT  
901 -----+-----+-----+-----+-----+-----+ 960  
CTTTTCTTCTTTATGTTAAGTACTTAAGTTTTTTAGTCGTTTCTGATGGGATTAGTTTTA  
298 K R R N T I H E F K K S A K T T L I K I 317  
AGATCCAGCACTGAAGATAAAAACCAAAAAAGTGAATACTGCAGACCAATGTGCTAATAG  
961 -----+-----+-----+-----+-----+-----+ 1020  
TCTAGGTCGTGACTTCTATTTTTGGTTTTTCACTTATGACGTCTGGTTACACGATTATC  
318 D P A L K I K T K K V N T A D Q C A N R 337  
ATGTACTAGGAATAAAGGACTTCCATTCACTTGCAAGGCTTTTGTTTTTGATAAAGCAAG  
1021 -----+-----+-----+-----+-----+-----+ 1080  
TACATGATCCTTATTTCTGAAGGTAAGTGAACGTTCCGAAAACAAAACTATTTCTGTTT  
338 C T R N K G L P F T C K A F V F D K A R 357  
AAAACAATGCCTCTGGTTCCCTTCAATAGCATGTCAAGTGGAGTGAAAAAGAATTTGG  
1081 -----+-----+-----+-----+-----+-----+ 1140  
TTTTGTTACGGAGACCAAGGGGAAGTTATCGTACAGTTCACCTCACTTTTTTCTTAAACC  
358 K Q C L W F P F N S M S S G V K K E F G 377  
CCATGAATTTGACCTCTATGAAAACAAAGACTACATTAGAACTGCATCATTGGTAAAGG  
1141 -----+-----+-----+-----+-----+-----+ 1200  
GGTACTTAAACTGGAGATACTTTTTGTTTCTGATGTAATCTTTGACGTAGTAACCATTTC  
378 H E F D L Y E N H D Y I R N C I I G K G 397

FIG.2b-2

FIG.2b-3

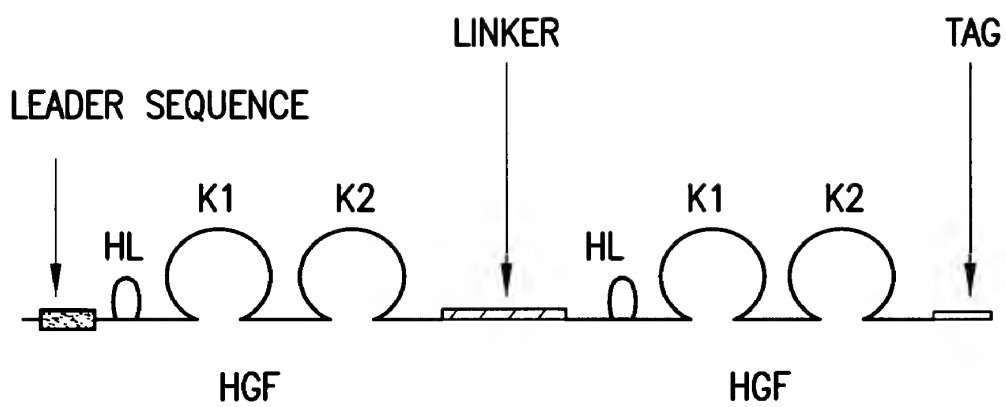


FIG.3a

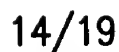


FIG.3b-1

FIG.3b-2



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1201 GACCTCTATGAAAACAAAGACTACATTAGAAACTGCATCATTGGTAAAGGACGCAGCTAC 1260  
-----+-----+-----+-----+-----+-----+  
CTGGAGATACTTTTGTCTGATGTAATCTTTGACGTAGTAACCATTTCCTGCGTCGATG  
392 D L Y E N K D Y I R N C I I G K G R S Y 411  
AAGGGAACAGTATCTATCACTAAGAGTGGCATCAAATGTCAGCCCTGGAGTTCATGATA  
1261 -----+-----+-----+-----+-----+-----+ 1320  
TTCCCTTGTCATAGATAGTGATTCTCACCGTAGTTTACAGTCGGGACCTCAAGGTACTAT  
412 K G T V S I T K S G I K C Q P W S S M I 431  
CCACACGAACACAGCTATCGGGGTAAAGACCTACAGGAAACTACTGTCGAAATCCTCGA  
1321 -----+-----+-----+-----+-----+-----+ 1380  
GGTGTGCTTGTGTCGATAGCCCCATTTCTGGATGTCCTTTTGATGACAGCTTTAGGAGCT  
432 P H E H S Y R G K D L Q E N Y C R N P R 451  
GGGGAAGAAGGGGGACCCTGGTGTTTCACAAGCAATCCAGAGGTACGCTACGAAGTCTGT  
1381 -----+-----+-----+-----+-----+-----+ 1440  
CCCCCTTCCCCCTGGGACCACAAAGTGTTCTGTTAGGTCTCCATGCGATGCTTCAGACA  
452 G E E G G P W C F T S N P E V R Y E V C 471  
GACATTCTCAGTGTTTCTGAGAAGTTGAATGCATGACCTGCAATGGGGAGAGTTATCGAGGT  
1441 -----+-----+-----+-----+-----+-----+ 1500  
CTGTAAGGAGTCACAAGTCTTCAACTTACGTACTGGACGTTACCCCTCTCAATAGCTCCA  
472 D I P Q C S E V E C M T C N G E S Y R G 491  
CTCATGGATCATAACAGAAATCAGGCAAGATTTGTCAGCGCTGGGATCATCAGACACCACAC  
1501 -----+-----+-----+-----+-----+-----+ 1560  
GAGTACCTAGTATGTCTTAGTCCGTTCTAAACAGTCGCGACCCTAGTAGTCTGTGGTGTG  
492 L M D H T E S G K I C Q R W D H Q T P H 511  
CGGCACAAATTCTTGCCTGAAAGATATCCCGACAAGGGCTTTGATGATAATTATTGCCGC  
1561 -----+-----+-----+-----+-----+-----+ 1620  
GCCGTGTTTAAGAACGGACTTTCTATAGGGCTGTTCCCGAACTACTATTAATAACGGCG  
512 R H K F L P E R Y P D K G F D D N Y C R 531  
AATCCCGATGGCCAGCCGAGGCCATGGTGCTATACTCTTGACCCTCACACCCGCTGGGAG  
1621 -----+-----+-----+-----+-----+-----+ 1680  
TTAGGGCTACCGGTCGGCTCCGGTACCACGATATGAGAACTGGGAGTGTGGGCGACCCTC  
532 N P D G Q P R P W C Y T L D P H T R W E 551  
TACTGTGCAATTAACATGCGCTGACAAAGCTGACGACGACGACAAACACCACCACCAC  
1681 -----+-----+-----+-----+-----+-----+ 1740  
ATGACACGTTAATTTTGTACGCGACTGTTTCGACTGCTGCTGCTGTTTGTGGTGGTGGT  
552 Y C A I K T C A D K A D D D D K H H H H 571  
CACCACCACTAGGGTCGAC  
1741 -----+----- 1759  
GTGGTGGTGATCCCAGCTG  
572 H H H \* 574

FIG.3b-3



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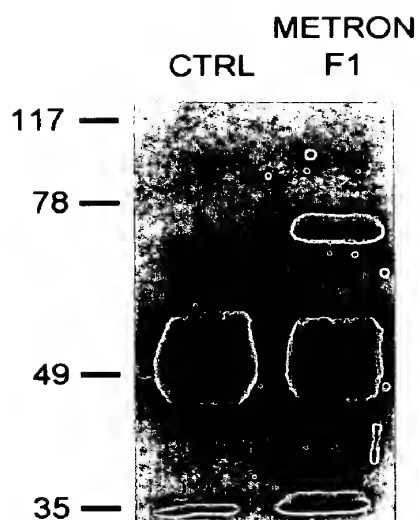


FIG.4

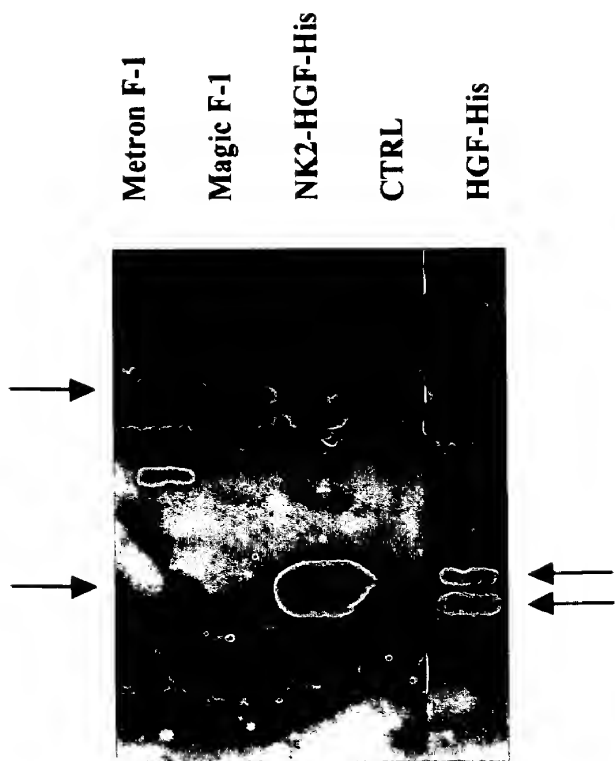


FIG.5a

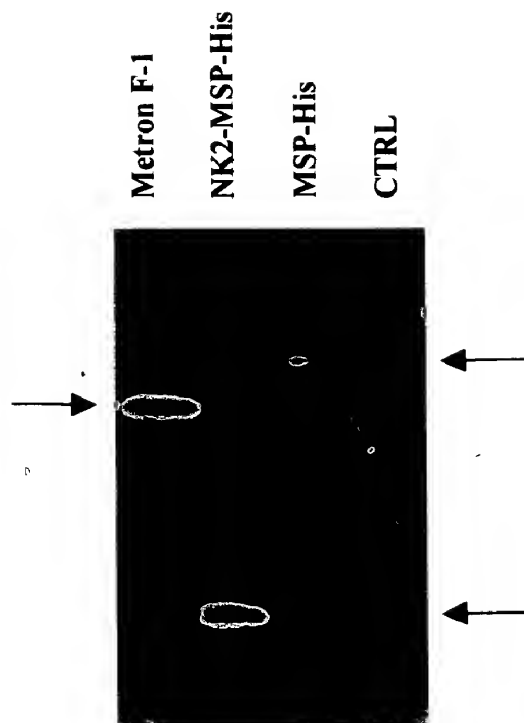


FIG.5b

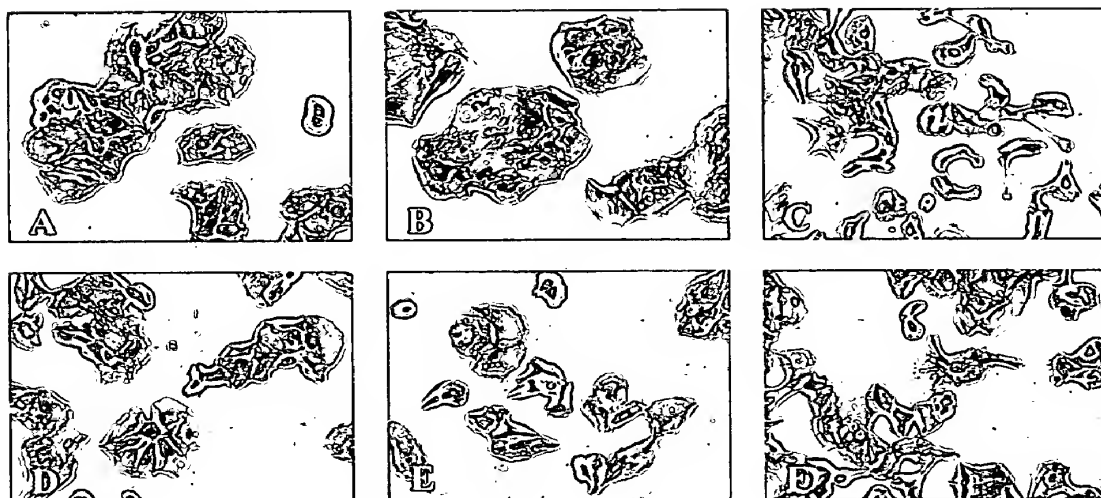


FIG.6

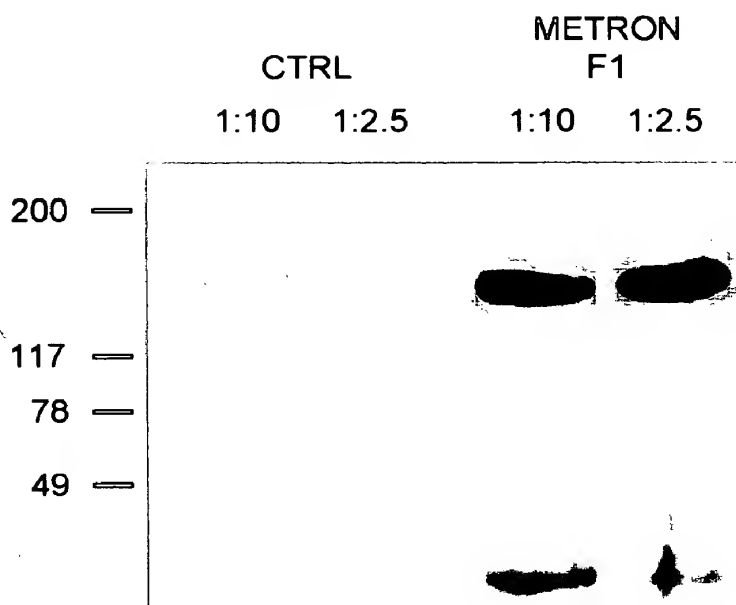


FIG.7

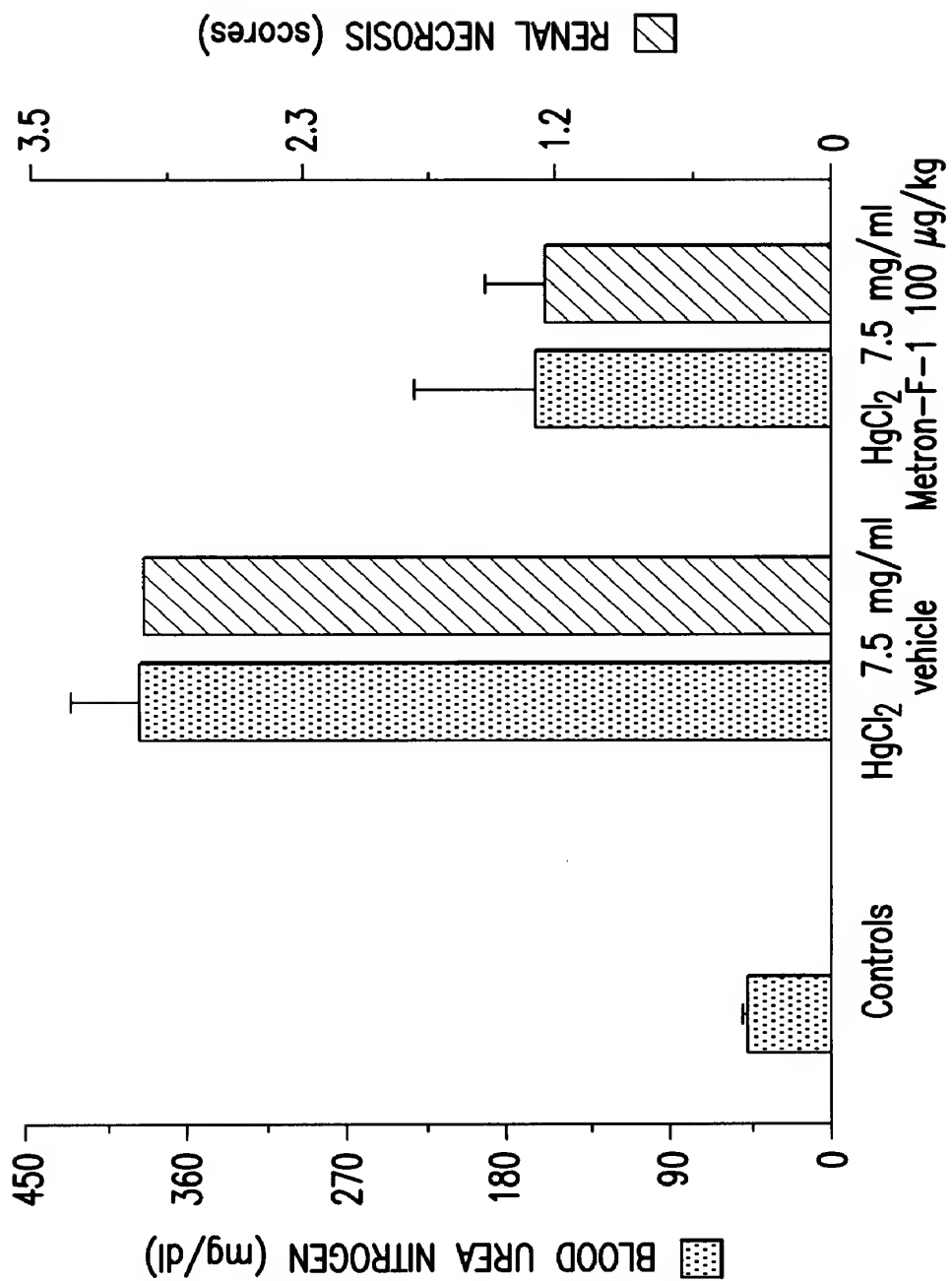


FIG.8